

1 ATGCTGTTCCGCGCCCGGGGCGGTACGGGGCAGGGGCTGGGGCGCGCGCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20
 61 CCCCCCGCGGGCGCTCGCGCCCTGGAGCCCCGCTGGATTGCTGCTGGGCGCTCGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40
 121 GGCTGCCAGCGGGCTGGGCTGGGGACCTGCCCTCCTCCTCCAGCGCGCGCTTCCTCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60
 181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTG 240
 61 C Q E K D Y H E E Y T E C D S S G S R W 80
 241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGG 300
 81 R V A I P N S A V D C S G L P D P V R G 100
 301 AAAGAATGCACTTTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120
 361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140
 421 GAATTGCCCGCAGGATTTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCCCTTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160
 481 GACAGCAGGCCAGACGGCTGTAACAACCTCTTCTGGATCCCTCGTGAAACTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180
 541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200
 601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220

FIG. 1A



661 AATGATCACTGCCAGGAGATGGACACCACCACTGACAAGTGGGTAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240

 721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260

 781 ACTACAGGCATCCTTATGGGTCTAAGCGGTCAAGCCTGTGCTGGTAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280

 841 ATTGAAGCGGTGGCGTACACATCAGAATGTTTTCTTGAAGCCAGGCACATTGAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300

 901 AAACCAGGTTTCACTCAACTGCCAGGTGTGTCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320

 961 AAAGAATGTATAAGGTGTAAAGACGACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340

 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360

 1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380

 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400

 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420

 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440

FIG. 1B



1321 TCGAATGTCCTTCCTGGCAACATGAAAACCTCCTGCTTCAATGTTGGAATTCAAAGTGC 1380
441 W N V L P G N M K T S C F N V G N S K C 460

1381 GATGGAATGAATGGTTGGGAGGTGGCTGCAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
461 D G M N G W E V A G D H I Q S G A G G S 480

1441 GACAATGATTACCTGATCTTAACTTGCATATCCAGGATTTAAACCACCAACATCTATG 1500
481 D N D Y L I L N L H I P G F K P P T S M 500

1501 ACTGGAGCCACGGGTCTGAACTAGGAAGAATAACATTTGCTTTGAGACCCTCTGTTCA 1560
501 T G A T G S E L G R I T F V F E T L C S 520

1561 GCTGACTGTGTTTTGTACTTCATGGTGCATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
521 A D C V L Y F M V D I N R K S T N V V E 540

1621 TCGTGGGGTGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
541 S W G G T K E K Q A Y T H I I F K N A T 560

1681 TTTACATTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTCATC 1740
561 F T F T W A F Q R T N Q G Q D N R R F I 580

1741 AATGACATGGTGAAGATTTATTCTATCACAGCCACTAATGCAGTTGATGGGGTGGCGTCC 1800
581 N D M V K I Y S I T A T N A V D G V A S 600

1801 TCATGCCGTGCCTGTGCCCTCGGTTCTGAACAGTGGGTTTCATCGTGTGTCCTCCCTGCCCT 1860
601 S C R A C A L G S E Q S G S S C V P C P 620

1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGAAGGAATGTCCACCTGACACCTAC 1920
621 P G H Y I E K E T N Q C K E C P P D T Y 640

1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATGCCGGCCTGGGAGTAAA 1980
641 L S I H Q V Y G K E A C I P C G P G S K 660

FIG. 1C



1981 AACAAATCAGGACCATTCCGGTTTGCATATAGTGAAGTCTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680

 2041 CAGATTTTGCATATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700

 2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

 2161 GAGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAAATA 2220
 721 E G K K M A L C T N N I T D F T V K E I 740

 2221 GTGGCAGGTCAGATGATTACACAAATTTGGTAGGGCATTGTATGCCACTCAACAATT 2280
 741 V A G S D D Y T N L V G A F V C Q S T I 760

 2281 ATTCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
 761 I P S E S K G F R A A L S S Q S I I L A 780

 2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAAGAAGAT 2400
 781 D T F I G V T V E T T L K N I N I K E D 800

 2401 ATGTTCCCAGTTCCAACAAGCCAAATACCAGATGTGCATTCTTTTATAAGTCTTCTACA 2460
 801 M F P V P T S Q I P D V H F F Y K S S T 820

 2461 GCAACAACATCTTGATTAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
 821 A T T S C I N G R S T A V K M R C N P T 840

 2521 AAATCTGGAGCAGGAGTGATTTTCACTCCCAGCAAGTGCCCAGCAGGTACCTGTGATGGG 2580
 841 K S G A G V I S V P S K C P A G T C D G 860

 2581 TGTACGTTCTATTTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACGGAGCATGAC 2640
 861 C T F Y F L W E S A E A C P L C T E H D 880

FIG. 1D



2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTTAGGAAACCTTGTATGTGTGGAAT 2700
 881 F H E I E G A C K R G F Q E T L Y V W N 900
 2701 GAACCTAAATGGTGCATTAAAGGAATTTCTTTGCCTGAGAAAAAGTTGGCAACCTGTGAA 2760
 901 E P K W C I K G I S L P E K K L A T C E 920
 2761 ACGGTTGACTTTTGGCTGAAGCTGGGAGCCCGTGTGGGAGCTTTTACTGCCGTTTTTGCTG 2820
 921 T V D F W L K V G A G V G A F T A V L L 940
 2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAGAAAAAGAAGACCATTTTGAAT 2880
 941 V A L T C Y F W K K N Q K K K K T I L N 960
 2881 CTGTTCAACTGAAAACTCAAGATCCCCAAATATATGAAGAGACAGTGTGTAGCCTTGA 2940
 961 L F N * 964
 2941 GACTAATGAACAAAGAAACCTGCTCTAGTTTTACAGGACCATATTTTAGGGTCTGTCCTC 3000
 3001 ATACCTGTCAATTGGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGGAAGGAGAT 3060
 3061 TGAAACATTTGATTGCCTTATCACATGGTCAACTACCTTGCCAAATAAAGGAAAGCAAAT 3120
 3121 GATTTGGGTCTCAACTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACAC 3180
 3181 ATAACTGAAAACCAAGTTTAAGCCCACCAATGCCTGCTGATGCATGCCATATAATTAAT 3240
 3241 GGGTAACTTTTATTCTTTATGATGTCTACATAACAAGTGTGATTGGAAGGCACATGTCA 3300
 3301 GCATATGCATTATGATCCAATTTATGTTTTTCTTTGTTTATATTTGGGGAAAATTAAA 3360
 3361 ATTTTTTTAAGGTAAAAA 3390

FIG. 1E



FIG. 2A

		10	20	30																												
1	M	L	F	R	A	R	G	E	V	R	G	R	G	E	A	E	A	P	R	R	G	R	S	F	F	W	S	TR16.aa				
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR			
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40			
		40	50	60																												
31	P	A	W	I	C	C	W	A	L	A	G	C	C	A	A	W	A	G	D	L	P	S	S	S	S	R	B	L	P	P	TR16.aa	
10	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
13	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		70	80	90																												
61	C	O	E	K	D	Y	H	F	E	Y	T	E	C	D	S	S	G	S	R	W	R	V	A	I	P	N	S	A	V	D	TR16.aa	
23	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
26	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		100	110	120																												
91	C	S	G	L	F	D	E	V	R	G	K	E	C	T	F	S	C	A	S	G	E	Y	L	E	M	K	N	Q	V	C	TR16.aa	
30	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
31	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		130	140	150																												
121	S	K	C	G	E	G	T	Y	S	L	G	S	G	I	K	F	D	E	W	D	E	L	P	A	G	E	S	N	I	A	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		160	170	180																												
151	T	F	M	D	T	V	V	G	P	S	D	S	R	P	D	G	C	N	N	S	S	W	I	P	R	G	N	Y	I	E	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		190	200	210																												
181	S	N	R	D	D	C	T	V	S	L	I	Y	A	V	H	L	K	R	S	G	Y	V	F	F	E	Y	Q	Y	V	D	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		220	230	240																												
211	N	N	I	F	F	E	F	F	I	O	N	D	O	C	O	E	M	D	T	T	T	D	R	W	V	K	L	T	D	N	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		250	260	270																												
241	G	E	W	G	S	H	S	V	M	L	K	S	G	T	N	I	L	Y	W	R	T	T	G	I	L	M	G	S	K	A	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		280	290	300																												
271	V	K	P	V	L	V	K	N	I	T	I	E	G	V	A	Y	T	S	E	C	P	E	C	K	P	G	T	F	S	N	TR16.aa	
51	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
43	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40
		310	320	330																												
301	K	P	G	S	F	N	C	O	V	C	P	R	N	T	Y	S	E	K	G	A	K	E	C	I	R	C	K	D	D	S	TR16.aa	
62	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
54	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAA53576.1 OX40

FIG. 2B

	340	350	360	
331	O F S G S S E C T E R P P C T T K D Y F Q I H T P C D E E G			TR16.aa
66	-			EMB
58	-			emb
	370	380	390	
361	K T O I M Y K W I E P K I C R E D L T D A I R L P P S G E K			TR16.aa
66	-			EMB
58	-			emb
	400	410	420	
391	K D C P P C N E G F Y N N G S S C H E C P P G T F S D G T			TR16.aa
70	T K C E R C P P H T Y T A I P N Y S N G C			EMB
62	T V C R E C G P G F Y N D V V S - S K E C			emb
	430	440	450	
421	K E C R P C P A G T E P A L G F E Y K W W N V L P G N M K T			TR16.aa
91	H Q C R K C - P T G S - - - - F D K V			EMB
82	K P C T W C N L R S G S - - - - E R K Q			emb
	460	470	480	
451	S C F N V G N S K C D C M N G W E V A G D H I Q S G A G G S			TR16.aa
105	K C T G T Q N S K C S C L P G W Y C A T D S S O T			EMB
98	L C T A T Q D T V C R C R A G - - - - T Q P L D S			emb
	490	500	510	
481	D N D Y L I L N L H I P G F K E P T S M T G A T G S E L G R			TR16.aa
130	-			EMB
119	-			emb
	520	530	540	
511	I T F V F E T L C S A D C V L Y F M V D I N R K S T N V V E			TR16.aa
132	-			EMB
122	-			emb
	550	560	570	
541	S W G G T K E K O A Y T H I I P R N A T F T F T W A F O R T			TR16.aa
137	-			EMB
127	-			emb
	580	590	600	
571	N O G O D N R R F I N D M V K I Y S I T A T N A V D G V A S			TR16.aa
137	-			EMB
127	-			emb
	610	620	630	
601	S C R A C A L G S E O S G S S C V P C P P G H Y I E K E T N			TR16.aa
141	-			EMB
128	-			emb

FIG. 2C

631	O C K E C P P D T Y L S P H O V Y G R E A C I P C G P G S K	TR16.aa	
147	----- G G I E M B	CAB41042.1 TNFR	
134	----- S P G e m b	CAA53576.1 OX40	
661	N N Q D H S V C Y S D C P P Y H E K E N O I L H Y D F S N L	TR16.aa	
150	D E Q G N P I C	EMB	CAB41042.1 TNFR
137	D N Q A C	emb	CAA53576.1 OX40
691	S S V G S L M N G P S P T S K G T K Y F H F P N I S L C G H	TR16.aa	
158	----- K S	C C V E M B	CAB41042.1 TNFR
142	----- K P W T N	C T L e m b	CAA53576.1 OX40
721	E G K R M A L C T N N I T D F T V K E I V A G S D D Y T N L	TR16.aa	
163	G E	EMB	CAB41042.1 TNFR
150	A G K H	emb	CAA53576.1 OX40
751	V G A F V C O S T I I P S E S K G F R A A L S S O S I I L A	TR16.aa	
166	----- C D	EMB	CAB41042.1 TNFR
166	----- C E D R D P E A T Q P Q E T Q G P P A R P I T V Q	emb	CAA53576.1 OX40
781	D T F I G V T V E T T L K N I N I K E D M F P V P T S O I P	TR16.aa	
168	-----	EMB	CAB41042.1 TNFR
191	P T	emb	CAA53576.1 OX40
811	D V H F P Y K S S T A T T S C I N G R S T A V K M R C N P T	TR16.aa	
168	-----	EMB	CAB41042.1 TNFR
203	----- S T R P V E V P G G R A V A A I L	emb	CAA53576.1 OX40
841	K S G A G V I S V P S K C P A G T C D G C T F Y F L W E S A	TR16.aa	
168	-----	EMB	CAB41042.1 TNFR
220	----- G L G L V	emb	CAA53576.1 OX40
871	E A C P L C T E H D F E E I E G A C K T G F O E T L Y V W N	TR16.aa	
168	-----	EMB	CAB41042.1 TNFR
229	----- G P L	emb	CAA53576.1 OX40
901	E P K W C I K G I S L E K K L A T C E T V D E W L K V G A	TR16.aa	
170	----- R N Y R L D P	EMB	CAB41042.1 TNFR
242	----- R D Q R L E P D A H K P	emb	CAA53576.1 OX40

FIG. 2D

		940		950		960																									
931	G	V	G	A	E	T	A	V	L	L	V	A	L	T	C	E	F	W	K	K	N	O	K	K	R	T	I	L	N	TR16.aa	
177	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	EMB	CAB41042.1 TNFR
255	G	G	G	S	F	R	T	P	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	emb	CAAS3576.1 OX40

961 L E N
184 K C - N
276 K I

TR16.aa
EMB CAB41042.1 TNFR
emb CAAS3576.1 OX40

TR16.aa

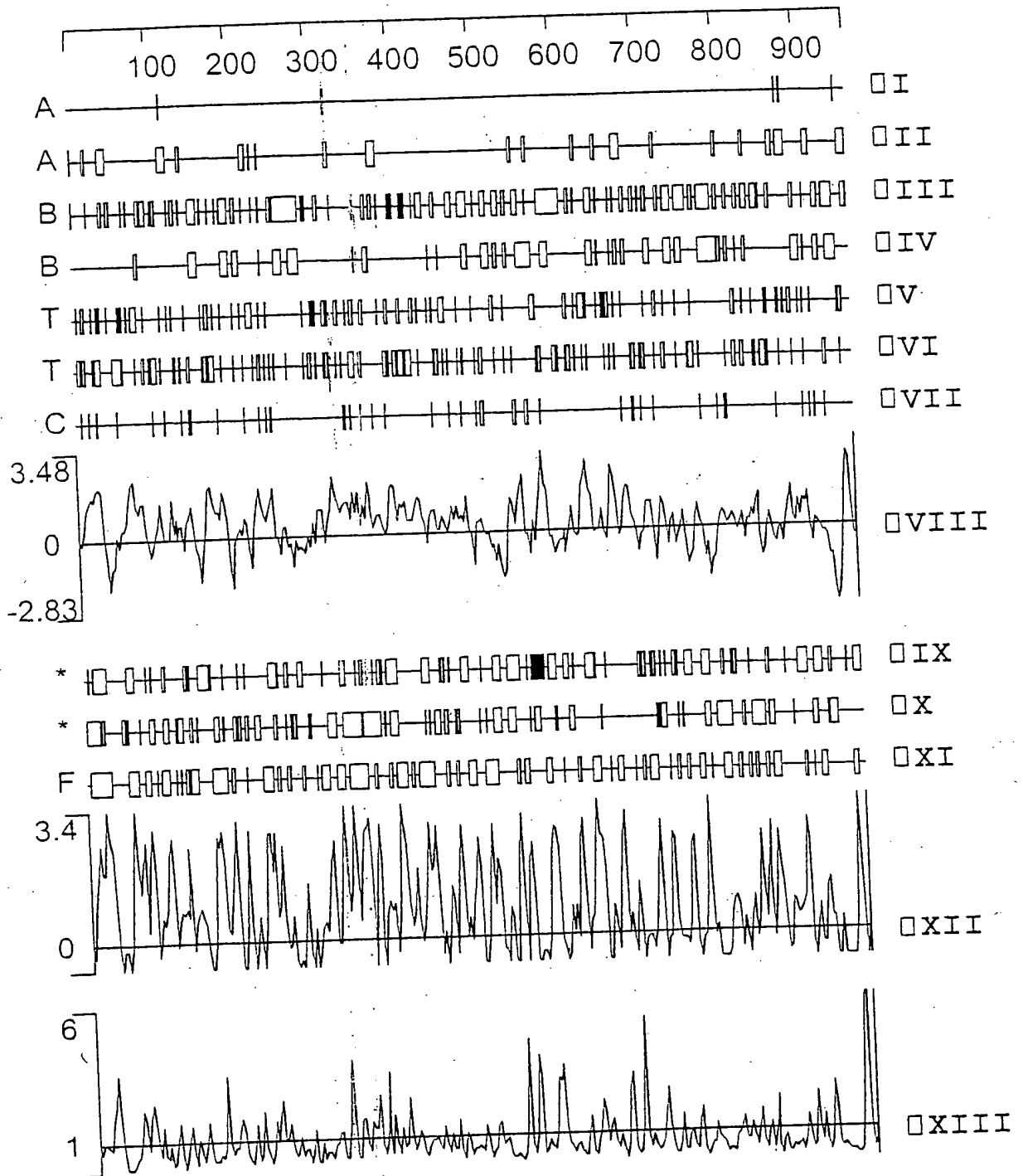


FIG. 3

1 ATGCTGTTCCGCGCCCGGGGCGGTACGGGGCAGCGGCTGGGGCGGCGCGGAGGCT 60
 1 M L F R A R G P V R G R G W G R P A E A 20
 61 CCCC GCCCGGGCGCTCGCCGCCCTGGAGCCCCCGCTGGATTGCTGCTGGGGCGCTCGCC 120
 21 P R R G R S P P W S P A W I C C W A L A 40
 121 GGCTGCCAGGCGGCTGGGCTGGGACCTGCCCTCCTCCTCCAGCGCGCGCTTCCTCCT 180
 41 G C Q A A W A G D L P S S S S R P L P P 60
 181 TGCCAGGAGAAAGATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGG 240
 61 C Q E K D Y H F E Y T E C D S S G S R W 80
 241 AGAGTTGCCATTCCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGC 300
 81 R V A I P N S A V D C S G L P D P V R G 100
 301 AAAGAATGCACTTTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGC 360
 101 K E C T F S C A S G E Y L E M K N Q V C 120
 361 AGTAAGTGTGGTGAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGAT 420
 121 S K C G E G T Y S L G S G I K F D E W D 140
 421 GAATTGCCGCGCAGGATTTTCTAACATCGCAACATTGACACTGTGGTGGGCCCTTCT 480
 141 E L P A G F S N I A T F M D T V V G P S 160
 481 GACAGCAGGCCAGACGGCTGTAACTCTTCTTGGATCCCTCGTGGAACACTACATAGAA 540
 161 D S R P D G C N N S S W I P R G N Y I E 180
 541 TCTAATCGTGATGACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGC 600
 181 S N R D D C T V S L I Y A V H L K K S G 200
 601 TATGTCTTCTTTGAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAA 660
 201 Y V F F E Y Q Y V D N N I F F E F F I Q 220
 661 AATGATCAGTGCCAGGAGATGGACACCACCACTGACAAGTGGGTAAACTTACAGACAAT 720
 221 N D Q C Q E M D T T T D K W V K L T D N 240

FIG. 4A



721 GGAGAATGGGGCTCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGA 780
 241 G E W G S H S V M L K S G T N I L Y W R 260
 781 ACTACAGGCATCCTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAATATCACA 840
 261 T T G I L M G S K A V K P V L V K N I T 280
 841 ATTGAAGGGGTGGCGTACACATCAGAATGTTTTCTTGCAGCCAGGCACATTAGCAAC 900
 281 I E G V A Y T S E C F P C K P G T F S N 300
 901 AAACCAGGTTTCATTCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCC 960
 301 K P G S F N C Q V C P R N T Y S E K G A 320
 961 AAAGAATGTATAAGGTGTAAAGACCACTCTCAATTTTCAGGATCCAGTGAGTGACAGAG 1020
 321 K E C I R C K D D S Q F S G S S E C T E 340
 1021 CGCCCTCCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGA 1080
 341 R P P C T T K D Y F Q I H T P C D E E G 360
 1081 AAGACACAGATAATGTACAAGTGGATAGAGCCCAAAATCTGCCGGGAGGATCTCACAGAT 1140
 361 K T Q I M Y K W I E P K I C R E D L T D 380
 1141 GCTATTAGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATT 1200
 381 A I R L P P S G E K K D C P P C N P G F 400
 1201 TATAACAATGGATCATCTTCTTGCCATCCCTGTCTCCTGGAACATTTTCAGATGGAACC 1260
 401 Y N N G S S S C H P C P P G T F S D G T 420
 1261 AAAGAATGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGG 1320
 421 K E C R P C P A G T E P A L G F E Y K W 440
 1321 TGAATGTCCTTCCTGGCAACATGAAAACCTCCTGCTTCAATGTTGGAATTCAAAGTGC 1380
 441 W N V L P G N M K T S C F N V G N S K C 460
 1381 GATGGAATGAATGGTTGGCAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCT 1440
 461 D G M N G W E V A G D H I Q S G A G G S 480

FIG. 4B



1441 GACAATGATTACCTGATCTTAACTTGCATATCCCAGGATTTAAACCACCAACATCTATG 1500
 481 D N D Y L I L M L H I P G F K P P T S M 500

 1501 ACTGGAGCCACGGGTTCTGAACTAGGAACAATAACATTTGTCTTTGAGACCCTCTGTTCA 1560
 501 T G A T G S E L G R I T F V F E T L C S 520

 1561 GCTGACTGTGTTTTGTACTTCATGCTGGATATTAATAGAAAAAGTACAAATGTGGTAGAA 1620
 521 A D C V L Y F M V D I N R K S T N V V E 540

 1621 TCGTGGGTGGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACT 1680
 541 S W G G T K E K Q A Y T H I I F K N A T 560

 1681 TTTACATTTACATGGGCATTCCAGAGAACTAATCAGGGTCAAGATAATAGACGGTTTCATC 1740
 561 F T F T W A F Q R T N Q G Q D N R R F I 580

 1741 AATGACATGGTGAAGATTTATTCTATCAGCCACTAATGCAGTTGATGGGTGGCGTCC 1800
 581 N D M V K I Y S I T A T N A V D G V A S 600

 1801 TCATGCCGTGCCCTGTGCCCTCGGTTCTGAACAGTCCGGTTCATCGTGTGCCCCCTGCCCT 1860
 601 S C R A C A L G S E Q S G S S C V P C P 620

 1861 CCAGGCCACTACATTGAGAAAGAAACCAACCAGTGCAGGAATGTCCACCTGACACCTAC 1920
 621 P G H Y I E K E T N Q C K E C P P D T Y 640

 1921 CTGTCCATACATCAGGTCTATGGCAAAGAGGCTTGTATTCCATCGGGCCTGGGAGTAAA 1980
 641 L S I H Q V Y G K E A C I P C G P G S K 660

 1981 AACAAATCAGGACCATTCGGTTTGTCTATAGTGAAGTCTTTTCTACCATGAAAAAGAAAAT 2040
 661 N N Q D H S V C Y S D C F F Y H E K E N 680

 2041 CAGATTTTGCATATGACTTTAGCAACCTCAGCAGTGTGGGCTCATTAAATGAATGGCCCC 2100
 681 Q I L H Y D F S N L S S V G S L M N G P 700

 2101 AGCTTCACCTCCAAAGGAACAAAATACTTCCATTTCTTCAATATCAGTTTATGTGGGCAT 2160
 701 S F T S K G T K Y F H F F N I S L C G H 720

FIG. 4C



2161 GAGGGGAAGAAGATGGCTCTCTGTACCAACAATATAACAGACTTTACAGTAAAAGAAATA 2220
 721 E G K K M A L C T N N I T D E T V K E I 740
 2221 GTGGCAGGGTCAGATGATTACACAAAATTTGGTAGGGGCATTGTATGCCAGTCAACAATT 2280
 741 V A G S D D Y T N L V G A F V C Q S T I 760
 2281 ATTCTTCTGAAAGTAAGGGTTTCCGAGCAGCCTTATCATCACAATCCATCATTCTGGCA 2340
 761 I P S E S K G F R A A L S S Q S I I L A 780
 2341 GATACATTCATAGGAGTCACAGTTGAAACCACATTGAAAAATATTAATATAAAACAAGAT 2400
 781 D T F I G V T V E T T L K N I N I K E D 800
 2401 ATGTTCCAGTTCCAACAAGCCAAATACCAGATGTGCATTCTTTTATAAGTCTTCTACA 2460
 801 M F P V P T S Q I P D V H F F Y K S S T 820
 2461 GCAACAACATCTTGTATTAAATGGCCGATCAACTGCTGTGAAAATGAGGTGTAATCCTACT 2520
 821 A T T S C I N G R S T A V K M R C N P T 840
 2521 AAATCTGGAGCAGGAGTGATTTTCAGTCCCCAGCAAGTGCCCAGCAGGTACCTGTGATGGG 2580
 841 K S G A G V I S V P S K C P A G T C D G 860
 2581 TGTACGTTCTATTTCTGTGGGAGAGTGCTGAAGCTTGCCCTCTGTGTACCGAGCATGAC 2640
 861 C T F Y F L W E S A E A C P L C T E H D 880
 2641 TTCCATGAGATTGAGGGAGCCTGCAAGAGAGGATTTTCAGGAAACCTTGATGTGTGGAAT 2700
 881 F H E I E G A C K R G F Q E T L Y V W N 900
 2701 GAACCTAAATGGTGCATTAAAGGAATTTCTTTGCCTGAGAAAAAGTTGCCAACCTGTGAA 2760
 901 E P K W C I K G I S L P E K K L A T C E 920
 2761 ACGGTTGACTTTTGGCTGAAGGTGGGAGCCGGTGTGGGAGCTTTTACTGCCGTTTTGCTG 2820
 921 T V D F W L K V G A G V G A F T A V L L 940
 2821 GTGGCTCTGACCTGCTACTTCTGAAAAAGAATCAAAAAGTGAATACAAATATTCCAAG 2880
 941 V A L T C Y F W K K N Q K L E Y K Y S K 960

FIG. 4D



2881 TTAGTAATGACGACTAACTCAAAGAGTGTGAACTCCCGGCTGCAGACAGTTGTGCTATC 2940
 961 L V M T T N S K E C E L P A A D S C A I 980
 2941 ATGGAAGGAGAAGATAATGAAGAGGAAGTTGTATATTCCAATAAACAGTCACTACTAGGA 3000
 981 M E G E D N E E E V V Y S N K Q S L L G 1000
 3001 AAACCTCAAATCTTTGGCAACCAAGCAAAAAGAACACCATTTTGAATCTGTTCAACTGAAA 3060
 1001 K L K S L A T K E K E D H F E S V Q L K 1020
 3061 ACCTCAAGATCCCCAAATATATGAAGAGACAGTGTAGCCTTGAGACTAATGAACAAA 3120
 1021 T S R S P N I * 1028
 3121 GAAACCTGCTCTAGTTTACAGGACCATATTTAGGGTCTGTCCTCATACCTGTCACATT 3180
 3181 GGTGATCTCACAGAGGAGGGCCATGCCGCTGAAAAGGAAGGAGATTGAAACATTTGATT 3240
 3241 GCCTTATCACATGGTCAAGTACCTTGCCAAATAAAGGAAAGCAAATGATTTGGGTCTCAA 3300
 3301 CTGAAGATGAAGCTCAACTCAGGAAGAGATTTATCTGTATATACACATAACTGAAAACCA 3360
 3361 AGTTTAAGCCCACCAATGCACTGCTGATGCATGCCATATAATTAATGGGTAACCTTTATT 3420
 3421 CTTTATGATGTCTACATAACAAGTGTGATTGGAAGCCACATGTGAGCATATGCATTATG 3480
 3481 ATCCAATTTATGTTTTTCTTTGTTTATATTTGGGAAAATTAAATTTTTTTAAGGTA 3540
 3541 AAAAAAAAAAAAAA 3556

FIG. 4E



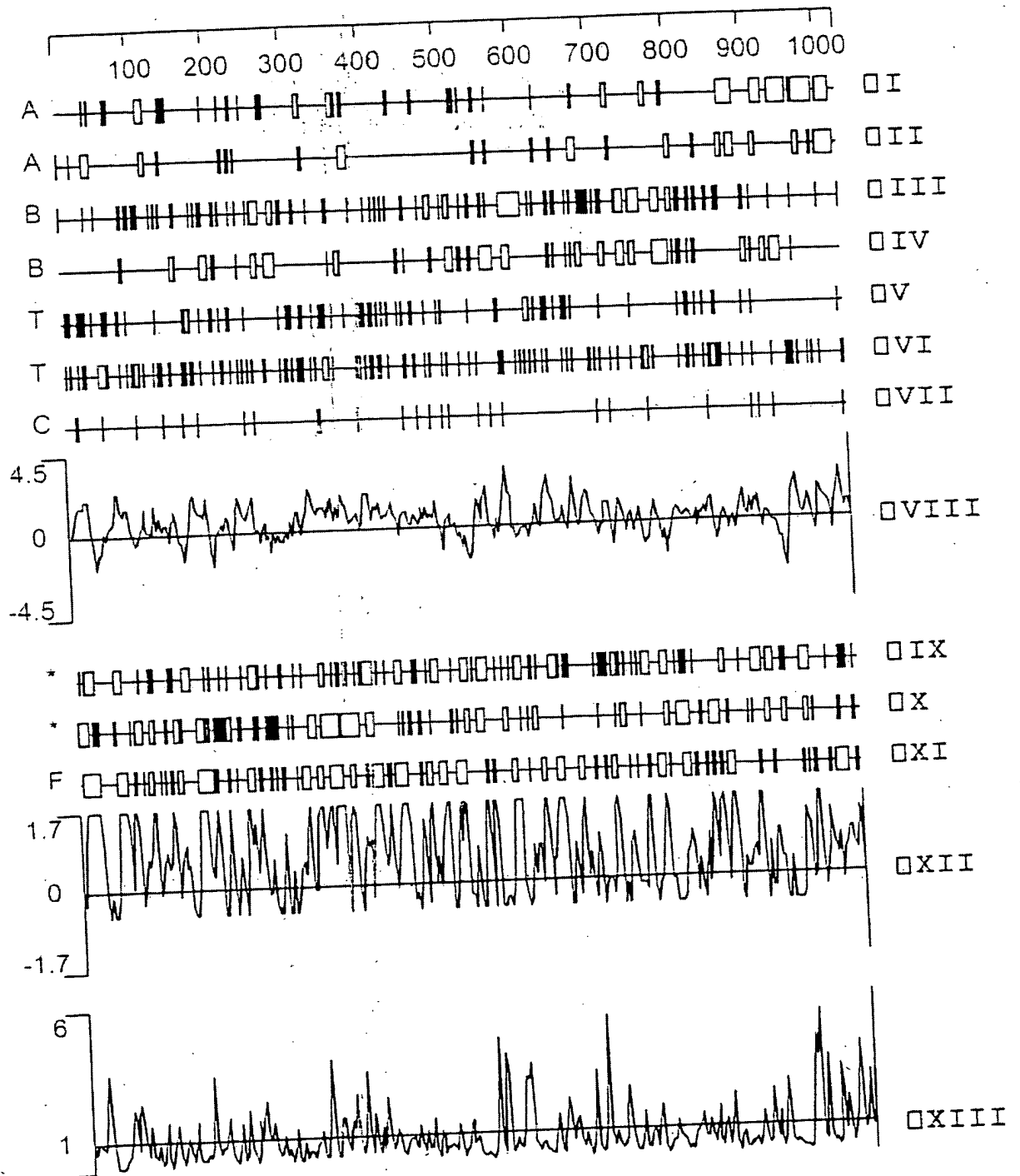


FIG. 5

	10	20	30	40	
1	MLFRARGPVVRGRGWGRPAEAPRRGRSPSPWS PAWICCWALA				SEQ ID 2
1	-----				SEC10
	50	60	70	80	
41	GCQAAWAGDLPSSSSRPLPPCQEKDYHFEYTECDSSGSRW				SEQ ID 2
1	-----				SEC10
	90	100	110	120	
81	RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLEMKNQVC				SEQ ID 2
1	-----MKNQVC				SEC10
	130	140	150	160	
121	SKCGEGTYSLGSGIKRDEWDELPAFESNIATFMDTVVGPS				SEQ ID 2
7	SKCGEGTYSLGSGIKRDEWDELPAFESNIATFMDTVVGPS				SEC10
	170	180	190	200	
161	DSRPDGCNNSSWIPRGNYESNRDDCTVSLIYAVHLKKS				SEQ ID 2
47	DSRPDGCNNSSWIPRGNYESNRDDCTVSLIYAVHLKKS				SEC10
	210	220	230	240	
201	YVFFEXQYVDNNIEFFEFQNDQCQEMDTTDDRKWKLT				SEQ ID 2
87	YVFFEXQYVDNNIEFFEFQNDQCQEMDTTDDRKWKLT				SEC10
	250	260	270	280	
241	GEWGSHSVMLKSGTNILYWRRTTGILMGSKAVKPVLVKNIT				SEQ ID 2
127	GEWGSHSVMLKSGTNILYWRRTTGILMGSKAVKPVLVKNIT				SEC10
	290	300	310	320	
281	IEGVAYTSECFFCKRGTFSNKPGEFNCQVCPRNTYSEKGA				SEQ ID 2
167	IEGVAYTSECFFCKRGTFSNKPGEFNCQVCPRNTYSEKGA				SEC10
	330	340	350	360	
321	KECIRCKDDSQFS -- GSSECTERPPCTTKDYFQIHTPCDE				SEQ ID 2
207	KECIRCKDDSQFS EE GSSECTERPPCTTKDYFQIHTPCDE				SEC10
	370	380	390	400	
359	EGKTQIMYKWIEPKICREDLTDAIRLPFSGEKKDCPPCNP				SEQ ID 2
247	EGKTQIMYKWIEPKICREDLTDAIRLPFSGEKKDCPPCNP				SEC10
	410	420	430	440	
399	GFYNNGSSSCHPCPPGTFSOGTKECRPCPAGTEPALGFY				SEQ ID 2
287	GFYNNGSSSCHPCPPGTFSOGTKECRPCPAGTEPALGFY				SEC10
	450	460	470	480	
439	KWWNVLPGNMRTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEQ ID 2
327	KWWNVLPGNMRTSCFNVGNSKCDGMNGWEVAGDHIQSGAG				SEC10
	490	500	510	520	
479	GSDNDYLLILNLHIPGKEPTSMGTGATGSELGRITVFETL				SEQ ID 2
367	GSDNDYLLILNLHIPGKEPTSMGTGATGSELGRITVFETL				SEC10

FIG. 6A



	530	540	550	560	
519	CSADCVLYEMVDINRKSTNVVSWGGTKEKQAYTHIIPKN				SEQ ID 2
407	CSADCVLYFMVDINRKSTNVVSWGGTKEKQAYTHIIPKN				SEC10
	570	580	590	600	
559	ATPTFTWAFQR TNQGQDNRRFINDMVKIYSITATNAVDGV				SEQ ID 2
447	ATPTFTWGI PR E - - - - -				SEC10
	610	620	630	640	
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECPD				SEQ ID 2
459	- - - - -				SEC10
	650	660	670	680	
639	TYLSIHQVYGKEACIPCGPGSKNNQDHSVCYSDCFFYHEK				SEQ ID 2
459	- - - - -				SEC10
	690	700	710	720	
679	ENQILHYDFS NLSSVGS L MN G P S F T S K G T K Y F H F F N I S L C				SEQ ID 2
459	- - - - - L I Q G R				SEC10
	730	740	750	760	
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYTNLVGAFVCQS				SEQ ID 2
464	- - - - -				SEC10
	770	780	790	800	
759	TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK				SEQ ID 2
464	- - - - -				SEC10
	810	820	830	840	
799	EDMFPVPTSQIPDVHFFYKSS TATTSCINGRSTAVKMRCN				SEQ ID 2
464	- - - - -				SEC10
	850	860	870	880	
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE				SEQ ID 2
464	- - - - -				SEC10
	890	900	910	920	
879	HDFHEIEGACKRGFQETLYVWNEPKWC IKGISLPEKKLAT				SEQ ID 2
464	- - - - -				SEC10
	930	940	950	960	
919	CETVDFWLKVGAGVGAF TAVLLVALTCYFWKKNQKKKKT I				SEQ ID 2
464	- - - - -				SEC10
959	LNLFN				SEQ ID 2
464	- - - - -				SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 6B



	10	20	30	40	
1	MLFRARGPVRGRGWGRPAZAPRRGRSPWPSPAWICCWALA				SEQ ID 4
1	-----				SEC10
	50	60	70	80	
41	GCQAAWAGDLPSSSSSRPLPPCQEKDYHFEYTECDSSGSRW				SEQ ID 4
1	-----				SEC10
	90	100	110	120	
81	RVAIPNSAVDCSGLPDPVRGKECTFSCASGEYLE				SEQ ID 4
1	-----				SEC10
	130	140	150	160	
121	SKCGEGTYSLSGSGIKFDEWDELPAGESNIATFMDTVVGPS				SEQ ID 4
7	SKCGEGTYSLSGSGIKFDEWDELPAGESNIATFMDTVVGPS				SEC10
	170	180	190	200	
161	DSRPDGCNNSSWIFRGNVIESNRDDCTVSLIYAVHLKKS				SEQ ID 4
47	DSRPDGCNNSSWIFRGNVIESNRDDCTVSLIYAVHLKKS				SEC10
	210	220	230	240	
201	YVFFEYQYVDNNIEFFEEFIQNDQCQEMDTTDDKWKLT				SEQ ID 4
57	YVFFEYQYVDNNIEFFEEFIQNDQCQEMDTTDDKWKLT				SEC10
	250	260	270	280	
241	GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT				SEQ ID 4
127	GEWGSHSVMLKSGTNILYWRTTGILMGSKAVKPVLVKNIT				SEC10
	290	300	310	320	
281	IEGVAYTSECFPCRPGTFSPNKPFGSPNCQVCPRNTYSE				SEQ ID 4
167	IEGVAYTSECFPCRPGTFSPNKPFGSPNCQVCPRNTYSE				SEC10
	330	340	350	360	
321	RECIRCKDDSQFS -- GSSECTERPPCTTKDYFQIHTPCDE				SEQ ID 4
207	RECIRCKDDSQFS EE GSSECTERPPCTTKDYFQIHTPCDE				SEC10
	370	380	390	400	
359	EGRTQIMYKWIIEPKICREDLTDAILRPPSGERKDCFP				SEQ ID 4
247	EGRTQIMYKWIIEPKICREDLTDAILRPPSGERKDCFP				SEC10
	410	420	430	440	
399	GFYNNGSSSCHFCPPGTFSDGTRECRPCFAGTEPALG				SEQ ID 4
287	GFYNNGSSSCHFCPPGTFSDGTRECRPCFAGTEPALG				SEC10
	450	460	470	480	
439	KWWNVLPGNMRTSCFNVGNSKCDGMNGWEVAGDHIQ				SEQ ID 4
327	KWWNVLPGNMRTSCFNVGNSKCDGMNGWEVAGDHIQ				SEC10
	490	500	510	520	
479	GSDNDYLLILNLHIEPGEKPPSTMTGATGSELGRITFV				SEQ ID 4
367	GSDNDYLLILNLHIEPGEKPPSTMTGATGSELGRITFV				SEC10

FIG. 7A



519	CSADCVLYFMVDINRKSTNVVSWGGTKEKQAYTHIIFKN	SEQ ID 4
407	CSADCVLYFMVDINRKSTNVVSWGGTKEKQAYTHIIFKN	SEC10
559	ATETETWAFQRTNQGGQDNRRFINDMVKIYSITATNAV DGV	SEQ ID 4
447	ATETETWGI PRE - - - - -	SEC10
599	ASSCRACALGSEQSGSSCVPCPPGHYIEKETNQCKECP PD	SEQ ID 4
459	- - - - -	SEC10
639	TYLSIHQVYGKEACIPCGPGSKNNQDHSVCYS DCFYHEK	SEQ ID 4
459	- - - - -	SEC10
679	ENQILHYDFS NLSSVGS LMN GPSFTSKG TKYFHHFNISLC	SEQ ID 4
459	- - - - - LIQ GP - - - - -	SEC10
719	GHEGKKMALCTNNITDFTVKEIVAGSDDYT NLVGAFVCQS	SEQ ID 4
464	- - - - -	SEC10
759	TIIPSESKGFRAALSSQSIILADTFIGVTVETTLKNINIK	SEQ ID 4
464	- - - - -	SEC10
799	EDMFPVPTSQIPDVHFFYKSS TATTSCINGRSTAVKMRCN	SEQ ID 4
464	- - - - -	SEC10
839	PTKSGAGVISVPSKCPAGTCDGCTFYFLWESAEACPLCTE	SEQ ID 4
464	- - - - -	SEC10
879	HDFHEIEGACKRGFQETLVVWNEPKWC IKGISLPEKKLAT	SEQ ID 4
464	- - - - -	SEC10
919	CETVDFWLKV GAGVGAF TAVLLVALTCYFWKKNQKLEYKY	SEQ ID 4
464	- - - - -	SEC10
959	SKLVMTTNSKECELPAA DSCAIMEGEDNEEEVVYSNKQSL	SEQ ID 4
464	- - - - -	SEC10
999	LGK LKSLATKEKEDHFESVQLKTSRSPNI	SEQ ID 4
464	- - - - - R	SEC10

Decoration 'Decoration #1': Shade (with solid black) residues that match the consensus named 'Consensus #1' exactly.

FIG. 7B

